



Replacement Sheet

Appl. No.: 10/667,462

Title: HUMAN LYSOPHOSPHATIDIC ACID

ACYLTRANSFERASE GAMMA-2

POLYPEPTIDE (As Amended)

Inventors: David W. LEUNG et al.

Atty. Docket No.: 077319-0382

**Figure 1A**

1 GGAAGTCAGCAGCGGTTGGGAGGGTGGCGGGAAATAGCGGGGGCAGC  
51 AGCCCCAGCCCTCAGAGAGACAGCAGAAAGGGAGGGAGGGGCTGCTGG  
101 GGGGACAGCCCCACCATTCCCTACCGCTATGGGCCAACCTCCCACTCC  
151 CACCTCCCCTCCATGGCCCCGGCTAGGGACACCCCCAAATCCCGTGGCC  
201 CCTTGCCACCGACACCCCCGACAGAGACAGAGACACAGGCCATCCGCCACCA  
251 CCGCTGCCGCAGCCCTGGCTGGGGAGGGGGCCAGCCCCCAGGGCCCTAC  
301 CCCTCTGAGGTGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG  
Met Asp Leu Trp Pro Gly Ala Trp  
343 ATG CTG CTG CTG CTG CTC TTC CTG CTG CTC TTC C  
Met Leu Leu Leu Phe Leu Leu Leu Phe L  
10  
20  
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG  
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys  
30

**Figure 1B**

418 TAC TTC TAC AAG ATG GCC TTC TAC AAT GGC TGG ATC C  
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG  
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C  
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

70

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA  
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

80

**Figure 1C**

568    GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C  
      Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G                  90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC  
      Iln Pro Tyr Val Val Ser Asn His Gln Ser Ser Leu                  100

643 GAT CTG CTT GGG ATG ATG GAG GTC CCA GGC CGC T  
      Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C                  120

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC  
      ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly                  110                  130

**Figure 1D**

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA CGA GTC ATC T  
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P  
140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC  
Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val  
150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G  
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V  
160

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC  
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His  
180

**Figure 1E**

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C  
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H  
190

905 ATT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA  
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile  
200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G  
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G  
210

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG  
Ilu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val  
220

230

**Figure 1E**

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G  
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A 240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG  
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met 250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G  
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G 270

1130 GT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG  
ly Gly Gly Asp Tyr Leu Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCCATCTGTCCCCATCTTCCTCCCC 290

1216 CACACCTACCCACCCAGTGGCCCTGAAGCAGGCCAAACCCCTCTTCCTT 300

1266 GtCTCCCCTCCCACTTATTCTCCCTTGAAATCTCAACTTCTGAA 310

**Figure 1G**

1316 GTGAATGTGGATAACAGGCCACTCCTGGCCCCCATCCATGG  
1366 ACTCTTGCCTCGGTGCAGTTCACTCTTGACCCCCACCTCCTACTGTC  
1416 TGTCTGGACAGTTGCCTCCACTCATCTCCAGTGACTCAGCCTACAC  
1466 AAGGGAGGGAAACATCCATCCCCCAGTGGAGTCTCCATTGTTGGA  
1516 CTCTACCCCTCTACCCCCACATGCCAGTGGACTCATCCATTGGA  
1566 ACAAATCCCCCCCCTCAAAGTCCATGGATTCAATGGACTCATCCATT  
1616 TGTGAGGGAACTTCTGCCCTCTGGCTGAAAGCTGATAACCTGAAGCACT  
1666 CCCAGGCTCATCCTGGAGGCTTCCCTCAGCACCTTCACTTCCCTCCAG  
1716 TGTAGCCCTCGTCAGTGGGGCTGGACCCCTTCTAAATTCAAGGGTCTCAT  
1766 GCCTGCCCTGCCAGATGCCAGGGTCACTCTGGATAACCAGT  
1816 TCAGTCTCCACATTTCTGGTTTCTGTCCCCATAGTACAGTTCTCAGTG  
1866 GACATGACCCCCACCCAGCCCCCTGCAGCCCCCTGCTGACCATCTCACCAGAC  
1916 ACAAGGGAAAGGAGACATCAGGTGCTGCACTCACTTCTGCCCTGG  
1966 GGAGTGGGAAACGAACCCCTGGCTGGAGGGATAAGGAGGGCTTTT

**Figure 1H**

2016 AATTATTCTTTCTGTTGAGGCTTCCCCCTCTGAGCCAGTTCA  
2066 TTTCTTCCTGGCATTAGCCACTCCCTGCC'CTCACTCCAGACCTGTT  
2116 CCCACAACTGGGAGGTAGGCTGGAGCAAAAGGAGGGTGGACCCAG  
2166 TTTTGCGTGGTTGGTTATTATAATTATCTGGATAACAGCAAAAAAACTG  
2216 AAAATAAAGAGAGAGAGAAAAAAA

**Figure 2A**

	10	20	30	40	50
Human LPAAT	1 <u>MDLWPGAWM-</u>	----- <u>LLLLF</u>	<u>LL-LLFLLPT</u>	<u>LMFCSPS</u> <u>AKY</u>	<u>F</u> ----- <u>EKMA</u>
Yeast LPAAT	1 <u>MSV-IGRFLY</u>	<u>YLRSVL-VVL</u>	<u>AL-AG</u> -----	----- <u>C</u> -----	----- <u>G</u> -----
E. coli LPAAT	1 <u>M</u> -----	----- <u>LYIF</u>	<u>RL-TITVIYS</u>	<u>ILVCVFGS</u> <u>TY</u>	-----
Maize LPAAT	1 <u>MAI-----</u>	----- <u>PLVLVV</u>	<u>PLGLFLLSG</u>	<u>LIVNAIQAVL</u>	<u>EVTIRPFSKS</u>
	60	70	80	90	100
Human LPAAT	51 <u>FYNGWILFLA</u>	<u>VLAIPVCAVR</u>	<u>GRNVENMKIL</u>	<u>RLMLLHIIKYL</u>	- <u>YGIRVEVRG</u>
Yeast LPAAT	51 <u>FY</u> ----- <u>G</u>	<u>VIASILCTLI</u>	<u>GKQHLAQWIT</u>	<u>ML_GLDV</u> ----- <u>K</u>	----- <u>VTAKKSL</u>
E. coli LPAAT	51 -----	----- <u>CLFS</u>	<u>PRNPKHVATF</u>	<u>GHMFGRLLAPL</u>	- <u>FGLKVECRK</u>
Maize LPAAT	51 <u>FYRRINRFLA</u>	<u>EL</u> -----	----- <u>L</u>	<u>WLQLVWVVDW</u>	<u>WAGVKVQLHA</u>
	110	120	130	140	150
Human LPAAT	101 AHHF-PPSQ-	- <u>PYVVVSNHQ</u>	<u>SSLDLGMME</u>	<u>VL</u> ----- <u>PGRC</u> ---	- <u>VPI-AKREL</u>
Yeast LPAAT	101 VVGE-ENLAK	<u>KPYIMIANHQ</u>	<u>STLDIFMLGR</u>	<u>IF</u> ----- <u>PPGCT</u> ---	----- <u>VTAKKSL</u>
E. coli LPAAT	101 PTDA-ESYG-	- <u>NATIYIANHQ</u>	<u>NNYDMVTASN</u>	<u>IVQ-PP</u> -----	<u>TVTV-GKKSL</u>
Maize LPAAT	101 DEETYRSMGK	<u>EHALIISNHR</u>	<u>SDIDWL-IGW</u>	<u>LLAQRSGLCG</u>	<u>STLAVMKSS</u>
	160	170	180	190	200
Human LPAAT	151 <u>LWAGSAGLAC</u>	<u>W---LAGVIF</u>	<u>IDRKRTGDAI</u>	<u>SVMSEVAQTL</u>	<u>LTQDVRVWV</u> -----
Yeast LPAAT	151 <u>KYVPPFLG</u> ---	<u>WEMALSGTYF</u>	<u>LDRSKRQEAI</u>	<u>DTLNKGLENV</u>	<u>KKNKRALWV</u> -----
E. coli LPAAT	151 <u>LWIPFFGQLY</u>	<u>W---LTGNLL</u>	<u>IDRNNRTKAH</u>	<u>GTIAEVVNHF</u>	<u>KKRRISIWM</u> -----
Maize LPAAT	151 <u>KFLPVIGWSM</u>	<u>WF---AEYLF</u>	<u>LERS-WAKDE</u>	<u>KTLKWGLQRL</u>	<u>KDFPRPFWLA</u>
	210	220	230	240	250
Human LPAAT	201 - <u>FPEGTRNHN</u>	<u>GS</u> -----	-----	<u>MLPFKRGAFH</u>	<u>LAVQAQVPIV</u>
Yeast LPAAT	201 - <u>FPEGTRSYT</u>	<u>SEL</u> -----	----- <u>T</u>	<u>MLPFKKGAFH</u>	<u>LAQQGKIPIV</u>
E. coli LPAAT	201 - <u>FPEGTRS</u> <u>RG</u>	<u>RGL</u> -----	-----	- <u>LPFKTGAFH</u>	<u>AAIAAGVPII</u>
Maize LPAAT	201 <u>LFVEGTRFTP</u>	<u>AKLLAAQEYA</u>	<u>ASQGLPAPRN</u>	<u>VLIPIRTKGFV</u>	<u>SAVSIIMRDFV</u>

**Figure 2 B**

Human LPAAT	251	<u>PIVMSSYQDF</u>	<u>YCKKERRFTS</u>	<u>GQCQVRVLPP</u>	<u>VPTEGLTPDD</u>	<u>VPALADR---</u>	
Yeast LPAAT	251	<u>PVVVSNTSTL</u>	<u>VSPKYGVFNR</u>	<u>GCMIVRILKP</u>	<u>ISTENLTKDK</u>	<u>TGEFAEK---</u>	
E. coli LPAAT	251	<u>PVCVSTTSNK</u>	<u>I--NLNRLHN</u>	<u>GLVIVEMLPP</u>	<u>IDVSQYGKDQ</u>	<u>VRELAHH---</u>	
Maize LPAAT	251	<u>PAIYDTT--V</u>	<u>IVPKDSDPQPT</u>	<u>MRLILKGQSS</u>	<u>VIHVRMKRHA</u>	<u>MSEMPKSDED</u>	
Human LPAAT	301	-----	<u>VRHSMLTV-F</u>	<u>REISTDGRGG</u>	<u>GDYLIKPGGG</u>	<u>G*</u>	
Yeast LPAAT	301	-----	<u>VRDOMVDT-L</u>	<u>KEIGGYSPANIN</u>	<u>DTTLPPQ---</u>		
E. coli LPAAT	301	-----	<u>CRSIMEQK-I</u>	<u>AELDKVEAE-</u>	<u>---REAAKG</u>	<u>V*</u>	
Maize LPAAT	301	VSKWCKDIFV	<u>AKDALLDKHL</u>	<u>ATGTFDEEIR</u>	<u>PIGRPVVKSLI</u>	<u>YTLFWSCLL</u>	
Human LPAAT	351	.....	.....	330	340	350	
Yeast LPAAT	351	--AIEY---	<u>A</u> <u>L</u> <u>---</u>	Q	HDKKVNNKKIK	<u>NEPVPSVSI</u>	<u>NDVNNTHNEG</u>
E. coli LPAAT	351	.....	.....	360	370	380	
Maize LPAAT	351	FGAIEFFKWT	<u>QLLSTWRGVA</u>	FTAGMALVT	<u>GVMHVFIMFS</u>	<u>QA</u> <u>---</u> <u>ERS</u>	
Human LPAAT	401	.....	.....	410	420	430	440
Yeast LPAAT	401	<u>S</u> <u>-----</u> <u>V</u>	<u>KKMH*</u>				
E. coli LPAAT	401	.....	.....				
Maize LPAAT	401	<u>SSARAARNRV</u>	<u>KKE*</u>				

## Replacement Sheet

Appl. No.: 10/667,462

Title: HUMAN LYSOPHOSPHATIDIC ACID

ACYLTRANSFERASE GAMMA-2

POLYPEPTIDE (As Amended)

Inventors: David W. LEUNG et al.

Atty. Docket No.: 077319-0382

**Figure 3A**

10	20	30	40	50	60
GGAGCGAGCT	GGGGGCGCG	TGGGGGCCG	GGCCCCCCA	TGGAGCTGTG	GCCGGTGTCTG
70	80	90	100	110	120
GCCGGGGCGC	TGCTGTTGCT	GCTGCTGCTG	GTGCAAGCTGA	GCCGGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAAGCTCG	CCCTGTACTG	CCCCCTGTGC	TTCACCGGTGT	CCGCCGTGGC	CTCCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGGC	CAGGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTCA	CGTCTCCAAC	CACCAAGAGCA	TCCTGGACAT	GATGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TtCCGGAGCG	CTGGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCTTCTTC	TCACCCGGCA	GGGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACACTGGC	GAGGGCATGG	TCAGGGAGAA	CCTCAAAAGTG

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**Figure 3B**

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAAACGAC	AATGGGGACC	TGCTGCCCTTT	TAAGAACGGC
610	620	630	640	650	660
GCCTTCTACC	TGGCACTCCA	GGCACACAGGTG	CCCATCGTCC	CCGTGGTGT	CTCTTCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAAACACCAA	GAAGAAAGTTTC	TTCACTTCAG	GAACAGTCAC	AGTGGAGGTG
730	740	750	760	770	780
CTGGAAAGCCA	TCCCCCACCAG	CGGCCCTCACT	GCGGGGGACG	TCCCTGGCCT	CGTGGACACC
790	800	810	820	830	840
TGCCAACCGGG	CCATGAGGAC	CACCTTCCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCCAC TGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCA CACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAAGC	CGATGGCTGG	AGGATGGCA	GAGGGACTC	CTCCCGGGCTT
970	980	990	1000	1010	1020
CCAATAACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGGAAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCCTGTC	ACT	ACAGGGCCCT	GCTGTCCCT	GCAGGGGGCT	CAGCTGGACC

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Figure 3C

1090	1100	1110	1120	1130	1140
CTCCCCGGGC	TCGAGGGCAG	GGACTCGCCGC	CCACGGCACCC	TCTGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGGGGCTGTG	GCCCCGCTGGT	GGGCTGAGCC	ACAAGGCC	CGATGGCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCCAGACT	CACGCCACCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGAA	TCGGGGCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGG	GTCAGGCAC
1330	1340	1350	1360	1370	1380
TACTCCGGTG	CTGTTTTTT	ATAAACACAC	TCTTGGAAAA	AAAAAAA	AAAAAAA
1390	1400	1410	1420	1430	1440
AAA.....	.....	.....	.....	.....	.....

Figure 4A

10            20            30            40            50  
GGAGCGAGCTGGCGGCCGTCCGGCGCCGGCCGCCCCGGCC ATG GAG CTC TGC CCG  
TGT CTC GCC GCG GCG CTC CTG TTG CTC CTC CTC GTC CTC CAG CTC  
Cys Leu Ala Ala Leu Leu Leu Leu Leu Val Gln Leu  
10            20            30            40            50  
60            70            80            90            100  
TGT CTC GCC GCG GCG CTC CTG TTG CTC CTC CTC GTC CTC CAG CTC  
Cys Leu Ala Ala Leu Leu Leu Leu Leu Val Gln Leu  
10            20            30            40            50  
100          110          120          130          140  
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC CTC TAC TGC GCG  
Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu Tyr Cys Ala  
10            20            30            40            50  
150          160          170          180          190  
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG CTC GTC TGC CTC CTG CTG  
Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys Leu Leu  
40            50            60            70            80  
190          200          210          220          230  
TGC CAC GGC GGC CGG ACC GTG GAG AAC ATG AGC ATC ATC GGC TGG  
Cys His Gly Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly Trp  
60

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#### **ACYLTRANSFERASE GAMMA-2**

**POLYPEPTIDE (As Amended)**

Inventors: David W. LEUNG et al.

**Figure 4 B**

TTC	GTG	CGA	AGC	TTC	AAG	TAC	TTT	TAC	GGG	CTC	CGC	TTC	GAG	GTG
Phe	Val	Arg	Ser	Phe	Lys	Tyr	Phe	Tyr	Gly	Leu	Arg	Phe	Glu	Val

280	290	300	310	320
CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC TGT GTC ATC GTC				
Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val				
90				

460	470	480	490	500
ATC AAC CGG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG	GAC			
Ile Asn Arg Gln Arg Ser Ser Thr Ala Met Thr Val Met	Ala	Asp		
			150	

Figure 4C

510	520	530	540	
CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT				
Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr				
160				170
550	560	570	580	590
CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CCT CCT TTT AAG				
Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys				
180				
600	610	620	630	640
AAG GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC				
Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val				
190				190
660	670	680	690	700
CCC GTG TAC TCT TCC TTC TCC TAC AAC ACC AAG AAG				
Pro Val Val Tyr Ser Ser Phe Ser Phe Tyr Asn Thr Lys Lys				
210				220
710	720			
AAG TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC				
Lys Phe Phe Thr Ser Gly Thr Val Gln Val Val Leu Glu Ala				
230				

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**Figure 4 D**

GAC	ACC	TGC	CAC	CGG	GCC	ATG	AGG	ACC	ACC	TTC	CTC	CAC	ATC	TCC
Asp	Thr	Cys	His	Arg	Ala	Met	Arg	Thr	Thr	Phe	Leu	His	Ile	Ser

870	880	890	900	910	920
CCG	CAG	TAG	CCCAGACCACGGCAGGGCATGACCTGGGAGGGCAGGTGGAAGC		
Pro	Ala	Gln	***		
940	950	960	970	980	
CGATGGCTTGGAGGAATGGGAGGGGACTCCTCCGGCTTCCTAAATTACCACTCTGTCCGG					

1000 1010 1020 1030 1040  
 CCCCCCAGCTCACTCAGCCCCGGAAGCAGGAAGCCCCCTTCTGTCACTGGTCTCAGAC  
 1050 1060 1070 1080 1090 1100  
 ACAGGCCCTGGTGTCCCCCTGCAGGGGCTCAGCTGGACCCCTCCCCGGGCTCGAGGCAG

**Figure 4 E**

1110	1120	1130	1140	1150	1160
	GGACTCGGCCACGGCACCTCTGGGNNGCTGGGNTGATAAAGATGAGGCTTGGCCTGTG				
1170	1180	1190	1200	1210	1220
	GCCCGCTGGCTGAGGCCACAAGGCCCGATGGCCAGGAGATGGGAGGGACCCC				
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAGTCCCCAGACTCACGGCACCCCTGGGCCACAGGGAGCCGGAAATGGGGCCTG				
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCTGGCCTGAAGAACCTCTGTGGGTCAAGCACTGTACTCCGTTGGCTGT				
1350	1360	1370	1380		
	ATAAACACACTCTTGAAAAAAAAAAAAAAAAA				

**Figure 5 A**  
 Alignment of LPAAT Sequences.

	10	20	30	40	50	
Human LPAAT- $\beta$	1	-----	-----	-----	-----	
Human LPAAT- $\alpha$	1	-----	-----	-----	-----	MEL WPC-----LA AALLLLLLV
Yeast LPAAT	1	-----	-----	-----	-----	MDL WPGCAWMLLL IFLLLLFLLP
E. coli LPAAT	1	-----	-----	-----	-----	MSV --IGRFLYYL RSVLWLLA
H. influenzae	1	-----	-----	-----	-----	-----
S. typhimurium	1	-----	-----	-----	-----	-----
L. douglasii	1	-----	-----	-----	-----	-----
C. nucifera	1	-----	-----	-----	-----	-----
	60	70	80	90	100	
Human LPAAT- $\beta$	51	QL--SRAAE FIAKVAL-YC ALCFTVSAVA	SLVCILLCHGG RTVENM-SI			
Human LPAAT- $\alpha$	51	TIWFCSSPSAK YFFKMAF-YN GWIILFIAVLA	TPVCAV--RG RNVENM-KIL			
Yeast LPAAT	51	G---CG--- FY-----	GVIA STLCTLICKQ HLAQWII-TAR			
E. coli LPAAT	51	M YI FRLITIVTYS IIVC--VFG SIYCLFSPRN PKHV--ATF				
H. influenzae	51	MKL LRIFMLIIC IIIC--VLG TIVSFIREKN PSNV--GIV				
S. typhimurium	51	M YI FRLITIVTYS IIVC--VFG SIYCLFSPRN PKHV--ATF				
L. douglasii	51	LLSC EKIFVCFAAFT VVLTAVAWG LIMWLLLPWP YMRLIRLGNLY				
C. nucifera	51	DRWITIVTYS VRIMACFL-- SMVTTIYWN MIMLILLPWP YARJRGONLY				

**Figure 5 B**

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Human LPAAT-β	110	<u>GWFVRSFKY</u> - -- <u>FYGCLRFEV</u> RDPRRLQEAR PCVIVSNHQ <b>S</b> ILLMMGIMMEV			
Human LPAAT-α	101	RLMILHIKY - --LYGIRVEV RGAIIHFPPSQ PYWVVSNHQS SLDLIGMMEV			
Yeast LPAAT	101	CFY-HVMKL - --MLGLDDMKV VGEENAK-K PYIMIANHQ <b>S</b> TLDIFMLCR <b>I</b>			
E. coli LPAAT	101	GHMFGR <b>L</b> --- APLFGLIKVEC RKPTDAE SYG NATYIYANHQ <b>N</b> NYDMVTLISM			
H. influenzae	101	ARWFGR <b>L</b> -FT YPLFGLKVEH RIPQDQKQ <b>S</b> RALYIYGNHQ <b>N</b> NYDMVTLISM			
S. typhimurium	101	GHMFGR <b>L</b> -FT APLFGLIKVEC RKPAADAENYG NATYIYANHQ <b>N</b> NYDMVTLISM			
L. douglassi	101	GHITIIGCNV-- IMYGIPIKI QGSEEHKK <b>R</b> A IFTYISN <b>H</b> AS PI DAAFFVMM			
C. nucifera	101	GHVTCRML <del>FT</del> MATTGNPITI EGSEFSNT <b>R</b> A I-YI CN <b>H</b> AS IV DIFELIMM <b>L</b>			
	110	120	130	140	150
	160	170	180	190	200
Human LPAAT-β	151	LP PERCVQ <b>L</b> A K RELLFLGPV- -GL DMVYLG <b>V</b> FEINRQRSS <b>T</b> AMT- VM <b>A</b> LL			
Human LPAAT-α	151	LP GRCVPI <b>A</b> K RELLWAGSA- -GLACWLAG <b>V</b> I FIDRKRT <b>G</b> D AIS- VM <b>S</b> EV			
Yeast LPAAT	151	FPPGCIVTA <b>K</b> KSLKVV <b>P</b> <b>F</b> <b>I</b> - -GWFMALSGT YFLDRSKRQE <b>A</b> ID- TLNK <b>G</b>			
E. coli LPAAT	151	VQPPTTV <b>G</b> <b>C</b> KSLIWIPPF - -GOLYWL <b>T</b> <b>G</b> N LL IDRNMR <b>T</b> <b>K</b> AHG- TIAEV			
H. influenzae	151	VQPPTTV <b>S</b> <b>G</b> <b>C</b> KSLIWIPPF TGILYWWV <b>G</b> N LL IDRNMR <b>T</b> <b>K</b> AHN- TMSQL			
S. typhimurium	151	VQPPTTV <b>G</b> <b>C</b> KSLIWIPPF TGOLYWL <b>T</b> <b>G</b> N LL IDRNMR <b>T</b> <b>K</b> AHS- TIAAV			
L. douglassi	151	APIGTVGV <b>A</b> <b>K</b> KEVWYPI <b>L</b> <b>G</b> Q-LYTIAH I RIDRSN PAA AIQSFMKEA			
C. nucifera	151	IPKGTV <b>T</b> <b>A</b> <b>K</b> KE II WYPLFG QFTLYVLANH QRIDRSN PAA AIES- IKEV			

**Figure 5C**

	210	220	230	240	250	
Human LPAAT- $\beta$ Human LPAAT- $\alpha$ Yeast LPAAT E. coli LPAAT H. influenzae S. typhimurium L. douglasii C. nucifera	201 <u>GERMRENLK</u> <u>VWLYPEGTRN</u> <u>DNGDL</u> — <u>LPF</u> <u>KKGAFYL</u> — <u>A</u> <u>VQAQVPIVPPV</u> 201 <u>AQTITIQDVR</u> <u>VWVFPEGTRN</u> <u>HNGSM</u> — <u>LPF</u> <u>KRGAFHL</u> — <u>A</u> <u>VQAQVPIVPPV</u> 201 <u>LENVKRNRA</u> <u>LWVFPEGTRS</u> <u>YTSELYMLPF</u> <u>KKGAFHL</u> — <u>A</u> <u>QQGKIPVPPV</u> 201 <u>VNHFKRRLS</u> <u>IWMFPEGTRS</u> <u>RGRGL</u> — <u>LPF</u> <u>KTGAF</u> — <u>HAA</u> <u>IAGVPIIPV</u> 201 <u>ARRINEDNLIS</u> <u>IWMFPEGTRN</u> <u>RGRGL</u> — <u>LPF</u> <u>KTGAFFHAA</u> <u>IAGVPIIPV</u> 201 <u>VNHFKRRLS</u> <u>IWMFPEGTRS</u> <u>RGRGL</u> — <u>LPF</u> <u>KTGAFFHAA</u> <u>IAGVPIIPV</u> 201 <u>VRVTEKNLIS</u> <u>LTMFPEGTRS</u> <u>GDGRL</u> — <u>LPF</u> <u>KKGFVHL</u> — <u>A</u> <u>LQSHLPIVPM</u> 201 <u>ARAWKKNLIS</u> <u>LITFPEGTRS</u> <u>KTGRL</u> — <u>LPF</u> <u>KKGFIHFTIA</u> <u>LQTRLPIVPM</u>					
	260	270	280	290	300	
Human LPAAT- $\beta$ Human LPAAT- $\alpha$ Yeast LPAAT E. coli LPAAT H. influenzae S. typhimurium L. douglasii C. nucifera	251 <u>VYSSFSS</u> — <u>F</u> <u>YNTKKKF</u> <u>FTS</u> <u>GIVTVQVLFA</u> <u>IPTSGLTAA</u> <u>D</u> <u>VPALVDTTCR</u> 251 <u>VMSSYQD</u> — <u>F</u> <u>YCKKERFTS</u> <u>GQQYVRVLP</u> <u>P</u> <u>VPTEGUTPDD</u> <u>VPALADRVRH</u> 251 <u>VVSNTST</u> — <u>L</u> <u>VSPKYGVFN</u> <u>GOMIVRILKP</u> <u>I</u> <u>STENLTTKDK</u> <u>I</u> <u>GEFAEKVRD</u> <u>CVSTIS</u> ---- 251 <u>NKDNILNRJHN</u> <u>GLVIVEMLP</u> <u>P</u> <u>IDVSOQGKDQ</u> <u>VRELAAHCR</u> <u>CVSSTH</u> ---- 251 <u>NKDNILNRWDN</u> <u>GKVLCIMDP</u> <u>P</u> <u>IDVSGGYTKDN</u> <u>VRDLAAYC</u> <u>CVSNTS</u> ---- 251 <u>NKVNMLNRINN</u> <u>GLVIVEMLP</u> <u>P</u> <u>VDVSEIGKDQ</u> <u>VRELAAHCRF</u> 251 <u>ILTGTTHLAWF</u> <u>TRKGIFRVRP</u> <u>VPIIVKYLPP</u> <u>P</u> <u>NTDDWTVK</u> <u>IDDXYVKMHD</u> <u>VLTGTHLAW</u> — <u>RKNQI</u> <u>RVRP</u> <u>APITVYKES</u> <u>P</u> <u>IKTDDWEEK</u> <u>INHYVEMDHF</u>					

**Figure 5D**

		310	320	330	340	350
Human LPAT-β	301 <u>AMRTTIFHIS</u>	KTPQENGATA	GSGVQPAQ*	-	-	-
Human LPAT-α	301 <u>SMTTVFREIS</u>	T <u>DGRGGDYL</u>	KRP <u>GGG</u> *	--	-	-
Yeast LPAT	301 <u>QMVDTILKEIG</u>	YSPA <u>INDTIL</u>	P <u>FQATEYAA</u> L	Q <u>HDKKVNKKI</u>	KNEPVS	VSI
E.coli LPAT	301 -S <u>IMEQKIAE</u>	<u>LDKEVA</u> - ER	<u>EAACKV</u> *	-	-	-
H.influenzae	301 <u>TLMERKIAE</u>	<u>LDEETIA</u> -	-	<u>KGN</u> *	-	-
S.typhimurium	301 <u>TALMEQKIAE</u>	<u>LDKEYVA</u> - ER	<u>EA<u>TGKV</u>*</u>	-	-	-
L.douglasii	301 T <u>YVRNIPASQ</u>	K <u>PLGS</u> -- <u>TNR</u> -	<u>S-K</u> *	-	-	-
C. nucifera	301 <u>TALYVTDHPE</u>	<u>SQKPLIVSKGR</u>	<u>DASGRNS</u> *	-	-	-
				360	370	380
						390
Human LPAT-β	351	-	-	-	-	-
Human LPAT-α	351	-	-	-	-	-
Yeast LPAT	351	SNDVNTNEG	SSVKKMH*	..	..	..
E.coli LPAT	351	-	-	-	-	-
H.influenzae	351	-	-	-	-	-
S.typhimurium	351	-	-	-	-	-
L.douglasii	351	-	-	-	-	-
C. nucifera	351	-	-	-	-	-

Figure 9 A

TCTATGAAACCAACATA	CATGGCGTTGCATCACAGT	TGGAGTCAGATGTGAGCCC	GGAG	60
GGCAGGTGTCTGGCTTG	CCACCCCGAACGCC	TGAGGGCAGCTGTTCCC	ACTGGCTCTGC	120
TGACCTTGTGCCTTGG	ACGGCTGCTCAGCGA	GAGGGCCGTGACCCG	CCTGAGCAGC	180
GCC ATG GGC CTG	CTG GCC TTC CTG AAG	ACC CAG TTC GTG CTG	CAC	225
Met Gly Leu Ala Phe	Leu Lys Thr Gln Phe	Val Leu His		
5	10			
CTG CTG GTC GGC TTT	GTC TTC GTG GTG AGT	GGT CTG GTC ATC AAC		270
Leu Leu Val Gly Phe	Val Phe Val Val Ser	Gly Leu Val Ile Asn		
15	20	25		
TTC GTC CAG CTG TGC	ACG CTG GCG CTC	TGG CCG GTC AGC AAG	CAG	315
Phe Val Gln Leu Cys	Thr Leu Ala Leu Trp	Pro Val Ser Lys Gln		
30	35	40		
CTC TAC CGC CGC CTC	AAC TGC CGC CTC GCA	TAC TCA CTC TGG AGC		360
Leu Tyr Arg Arg Leu	Asn Cys Arg Leu Ala	Tyr Ser Leu Trp Ser		
45	50	55		
CAA CTG GTC ATG CTG	CTG GAG TGG TGG TCC	TGC ACG GAG TGT ACA		405
Gln Leu Val Met Leu	Leu Glu Trp Trp Ser	Cys Thr Glu Cys Thr		
60	65	70		
CTG TTC ACG GAC CAG	GCC ACG GTA GAG CGC	TTT GGG AAG GAG CAC		450
Leu Phe Thr Asp Gln	Ala Thr Val Glu Arg	Phe Gly Lys Glu His		
75	80	85		
GCA GTC ATC ATC CTC	AAC CAC AAC TTC GAG ATC	GAC TTC CTC TGT		495
Ala Val Ile Ile Leu	Asn His Asn Phe Glu	Ile Asp Phe Leu Cys		
90	95	100		
GGG TGG ACC ATG TGT	GAG CGC TTC GGA GTG CTG	GGG AGC TCC AAG		540
Gly Trp Thr Met Cys	Glu Arg Phe Gly Val	Leu Gly Ser Ser Lys		
105	110	115		
GTC CTC GCT AAG AAG	GAG CTG CTC TAC GTG	CCC CTC ATC GGC TGG		585
Val Leu Ala Lys Lys	Glu Leu Leu Tyr Val	Pro Leu Ile Gly Trp		
120	125	130		
ACG TGG TAC TTT CTG	GAG ATT GTG TTC TGC	AAG CGG AAG TGG GAG		630
Thr Trp Tyr Phe Leu	Glu Ile Val Phe Cys	Lys Arg Lys Trp Glu		
135	140	145		
GAG GAC CGG' GAC ACC	GTG GTC GAA GGG CTG	AGG CGC CTG TCG GAC		675
Glu Asp Arg Asp Thr	Val Val Glu Gly Leu	Arg Arg Leu Ser Asp		
150	155	160		
TAC CCC GAG TAC ATG	TGG TTT CTC CTG TAC	TGC GAG GGG ACG CGC		720
Tyr Pro Glu Tyr Met	Trp Phe Leu Leu Tyr	Cys Glu Gly Thr Arg		
165	170	175		
TTC ACG GAG ACC AAG	CAC CGC GTT AGC ATG	GAG GTG GCG GCT GCT		765
Phe Thr Glu Thr Lys	His Arg Val Ser Met	Glu Val Ala Ala Ala		
180	185	190		
AAG GGG CTT CCT GTC	CTC AAG TAC CAC CTG	CTG CCG CGG ACC AAG		810
Lys Gly Leu Pro Val	Leu Lys Tyr His Leu	Leu Pro Arg Thr Lys		
195	200	205		
GGC TTC ACC ACC GCA	GTC AAG TGC CTC CCG	GGG ACA GTC GCA GCT		855
Gly Phe Thr Thr Ala	Val Lys Cys Leu Arg	Gly Thr Val Ala Ala		
210	215	220		
GTC TAT GAT GTA ACC	CTG AAC TTC AGA GGA	AAC AAG AAC CCG TCC		900
Val Tyr Asp Val Thr	Leu Asn Phe Arg Gly	Asn Lys Asn Pro Ser		
225	230	235		
CTG CTG GGG ATC CTC	TAC GGG AAG AAG TAC	GAG GCG GAC ATG TGC		945
Leu Leu Gly Ile Leu	Tyr Gly Lys Lys Tyr	Glu Ala Asp Met Cys		
240	245	250		
GTG AGG AGA TTT CCT	CTG GAA GAC ATC CCG	CTG GAT GAA AAG GAA		990
Val Arg Arg Phe Pro	Leu Glu Asp Ile Pro	Leu Asp Glu Lys Glu		
255	260	265		
GCA GCT CAG TGG CTT	CAT AAA CTG TAC CAG	GAG AAG GAC GCG CTC		1035

**Figure 9B**

Ala Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu			
270	275	280	
CAG GAG ATA TAT AAT CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT			1080
Gln Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe			
285	290	295	
AAG CCT GCC CGG AGG CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG			1125
Lys Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp			
300	305	310	
GCC ACC ATT CTC CTG TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC			1170
Ala Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val			
315	320	325	
TTT GCC AGC GGA TCA CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT			1215
Phe Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe			
330	335	340	
GTG GGA GCA GCT TCC TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT			1260
Val Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Val Thr			
345	350	355	
GAG ATA GAA AAA GGC TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA			1305
Glu Ile Glu Lys Gly Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys			
360	365	370	
AAG GAA TAA TTAATGGCTGTGACTAACACACAGCGGCCCTGACGGTGGTATCCAGTT			1362
LYS Glu ***			
AACTCAAAACCAACACACAGAGTCAGGAAAAGACAATTAGAAACTATTTCTTATTAA			1422
CTGGTACTAATATTAACAAACTTGAGCCAAGAGTAAGAATTCAAAGGCCTGTCAGG			1482
TGAAGTCTTCAGCCTCCCACAGCGCAGGGTCCAGCATCTCACGCGGCCGTGGGAGG			1542
TGGGTCCGGCCGGAGAGGCCCTCCCGCGGACGCCGTCTCCAGAACTCCGTTCCAAGAG			1602
GGACCTTGGCTGTTCTCTCCTAAACTAGATCAAATTTAAAAAAAAAAAAAA			1660

**Figure 10 A**

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCTCAACTGCCGCCCTGCC	61
TACTCACTCTGGAGCCTAGCACAAACTAGAACCAACGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCTCTGGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTAAGCGAAAAAGGAAGTATAACAACAAAGTCCATAACTGGTC	238
Met Leu	
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

Replacement Sheet  
Appl. No.: 10/667,462

Title: HUMAN LYSOPHOSPHATIDIC ACID  
ACYLTRANSFERASE GAMMA-2  
POLYPEPTIDE (As Amended)

Inventors: David W. LEUNG et al.  
Atty. Docket No.: 077319-0382

**Figure 10 B**

260	265	270	
CCT CTC CTG ATC CTG ACT TTC	TTG GGG TTT GTG GGA	GCA GCT TCC	1093
Pro Leu Leu Ile Leu Thr Phe	Leu Gly Phe Val Gly	Ala Ala Ser	
275	280	285	
TTT GGA GTT CGC AGA CTG ATA	GGA GTA ACT GAG ATA	GAA AAA GGC	1138
Phe Gly Val Arg Arg Leu Ile	Gly Val Thr Glu Ile	Glu Lys Gly	
290	295	300	
TCC AGC TAC GGA AAC CAA GAG	TTT AAG AAA AAG GAA TAA	TTAATGGC	1185
Ser Ser Tyr Gly Asn Gln Glu	Phe Lys Lys Lys	Glu ***	
305	310		
TGTGACTGAACACACCGCGGCCCTGACGGTGGTATCCAGTTAACTCAAACCAACACACAG			1245
AGTGCAAGAAAAGACAATTAGAAAATTAGTTCTTATTAACTGGTGACTAATATTAAACAA			1305
AACTTGAGCCAAGAGTAAAGAATTCAAGAAGGCCCTGTCAGGTGAAGTCTTCAGCCTCCCAC			1365
AGCGCAGGGTCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC			1425
TCCCGGGACGCCGTCTCCAGAACCTCGCTTCAAGAGGGACCTTGGCTGCTTCTC			1485
TCCTTAAACTTAGATCAAATTTAAAAAAAAAAAAAA			1523

Figure 11A

TGAACCCAGCGGCTCCATCTCAGCTTCTGGTTCTAAAGTCCATGTGCCAAAGGCTGCCAG	5	61
GAAGGAGACGCCCTCCTGAGTCCTGGATCTTCTTCTGGAAATCTTGACTGTGGG	10	121
<u>TAGTTATTCTGAATAAGAGCGTCCACGCATC</u>	15	175
ATG GAC CTC GCG GGA CTG	20	
Met Asp Leu Ala Gly Leu	25	
CTG AAG TCT CAG TTC CTG TGC CAC CTG GTC TTC TGC TAC GTC TTT	30	220
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe	35	
10 15 20	40	
ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC	45	265
Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe Thr Leu	50	
25 30 35	55	
CTC CTC TGG CCC ATT AAC AAG CAG CTC TTC CGG AAG ATC AAC TGC	60	310
Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys Ile Asn Cys	65	
40 45 50	70	
AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG	75	355
Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu	80	
55 60 65	85	
TGG TGG TCG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC	90	400
Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala	95	
70 75 80	100	
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC	105	445
Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His	110	
85 90 95	115	
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC	120	490
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg	125	
100 105 110	130	
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG	135	535
Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu	140	
115 120 125	145	
GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG	150	580
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met	155	
130 135 140	160	
GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC	165	625
Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala	170	
145 150 155	175	
ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TAT TTT TTC	180	670
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe	185	
160 165 170	190	
CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG	195	715
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu	200	
175 180 185	190	
ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG	205	760
Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys	210	
190 195 200	210	
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG	215	805
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg	220	
205 210 215	220	
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT	225	850
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn	230	
210 215 220	220	
TTC AGA AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA	240	895
Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	245	
235 240 245	250	
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA	255	940
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu	260	
245 250 255	250	
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG	270	985
Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	275	
265 270 275		

**Figure 11B**

CTC TAC CAG GAG AAG GAT GCC TTT CAG GAG GAG TAC TAC AGG ACG	1030
Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr Tyr Arg Thr	
280 285 290	
GGC ACC TTC CCA GAG ACG CCC ATG GTG CCC CCC CGG CGG CCC TGG	1075
Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg Pro Trp	
295 300 305	
ACC CTC GTG AAC TGG CTG TTT TGG GCC TCG CTG GTG CTC TAC CCT	1120
Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr Pro	
310 315 320	
TTC TTC CAG TTC CTG GTC AGC ATG ATC AGG AGC GGG TCT TCC CTG	1165
Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu	
325 330 335	
ACG CTG GCC AGC TTC ATC CTC GTC TTC TTT GTG GCC TCC GTG GGA	1210
Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly	
340 345 350	
GTT CGA TGG ATG ATT GGT GTG ACG GAA ATT GAC AAG GGC TCT GCC	1255
Val Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala	
355 360 365	
TAC GGC AAC TCT GAC AGC AAG CAG AAA CTG AAT GAC TGA CTCAGGG	1301
Tyr Gly Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp ***	
370 375	
AGGTGTCACCATCCGAAGGGAACCTTGGGGAACTGGTGGCCTCTGCATATCCTCCTTAGT	1361
GGGACACGGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGACCTCT	1421
CCAGCCAGGGAGTCGGTCTCAAGGCCGATGGGGAGGAAGATGTTTGTAAATCTTTTT	1481
TCCCCATGTGCTTTAGTGGGCTTGGTTCTTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGGA	1541
GTGTGGTAGTGTGAACTTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGGA	1601
GGGCAGGGCTGGGGACCGAAGGGACAAGTCCCCCTTCATCCTTGTTGCTGAGTTTC	1661
TGTAACCCCTGGTTGCCAGAGATAAAGTGAAAAGTGTCTTAGGTGAGATGACTAAATTAT	1721
GCCTCCAAGAAAAAAAAATTAAAGTGTCTGGGTCAAAAAAAA	1774